The Distribution of Chromosomal Aberrations in Human Cells Predicted by a Generalized Time-Dependent Model of Radiation-Induced Formation of Aberrations

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New experimental data show how chromosomal aberrations for low- and high-LET radiation are dependent on DSB repair deficiencies in wild-type, AT and NBS cells. We simulated the development of chromosomal aberrations in these cells lines in a stochastic track-structure-dependent model, in which different cells have different kinetics of DSB repair. We updated a previously formulated model of chromosomal aberrations, which was based on a stochastic Monte Carlo approach, to consider the time-dependence of DSB rejoining. The previous version of the model had an assumption that all DSBs would rejoin, and therefore we called it a “time-independent” model. The chromosomal-aberrations model takes into account the DNA and track structure for low- and high-LET radiations, and provides an explanation and prediction of the statistics of rare and more complex aberrations. We compared the program-simulated kinetics of DSB rejoining to the experimentally-derived bimodal exponential curves of the DSB kinetics. We scored the formation of translocations, dicentrics, acentric and centric rings, deletions, and inversions. The fraction of DSBs participating in aberrations was studied in relation to the rejoining time. Comparisons of simulated dose dependence for simple aberrations to the experimental dose-dependence for HF19, AT and NBS cells will be made.